RF Errors Corrected by the STIC stems Branch

1652

CRF Processing Date: 12/7/2000

Edited by:

Verified by: _____ (STIC staff

Serial Number: 09/492,029 ENTERED

RECEIVED #9

DEC 21 2000

☐ Changed a file from non-ASCII to ASC

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically: _____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included: _____

☐ Deleted extra, invalid, headings used by an applicant, specifically: _____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____.

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically: _____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically: _____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☑ Other: Seq 2 - corrected (222) response

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/492,029

DATE: 12/18/2000
TIME: 15:05:02

Input Set : A:\Pto.amc
Output Set: N:\CRF3\12182000\I492029.raw

<110> APPLICANT: Zuker, Charles S.
Adler, Jon Elliot
Lindemeier, Juergen
The Regents of the University of California
<120> TITLE OF INVENTION: Assays for Sensory Modulators Using a Sensory Cell Specific G-Protein Beta Subunit
<130> FILE REFERENCE: 02307E-092710US
<140> CURRENT APPLICATION NUMBER: US 09/492,029
<141> CURRENT FILING DATE: 2000-01-26
<150> PRIOR APPLICATION NUMBER: US 60/117,404
<151> PRIOR FILING DATE: 1999-01-27
<160> NUMBER OF SEQ ID NOS: 5
<170> SOFTWARE: PatentIn Ver. 2.1
<210> SEQ ID NO: 1
<211> LENGTH: 156
<212> TYPE: DNA
<213> ORGANISM: Rattus sp.
<220> FEATURE:
<223> OTHER INFORMATION: rat tongue circumvallate papillae taste receptor cell cDNA clone 165-17
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<210> SEQ ID NO: 2
<211> LENGTH: 1520
<212> TYPE: DNA
<213> ORGANISM: Rattus sp.
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (78)..(1097)
<223> OTHER INFORMATION: rat taste cell specific G-protein beta 3 subunit (TC-Gbeta3)
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Met Gly Glu Met Glu Gln Leu Lys Gln Glu Ala
1 5 10
gag cag ctc aag aag cag att gct gat gcc agg aaa gcc tgt gcg gac 158
Glu Gln Leu Lys Lys Gln Ile Ala Asp Ala Arg Lys Ala Cys Ala Asp
15 20 25
atc act ctg gct gag ctt gtg tct ggc ctg gag gtg gtg gga cga gtc 206
Ile Thr Leu Ala Glu Leu Val Ser Gly Leu Glu Val Val Gly Arg Val
30 35 40
cag atg cgg aca cgg agg acg tta agg gga cac ctg gct aag atc tat 254
Gln Met Arg Thr Arg Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr
45 50 55

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72 gat ggg aag ctg atc gtg tgg gac act tac acc acc aat aag gtg cat   350
73 Asp Gly Lys Leu Ile Val Trp Asp Thr Tyr Thr Thr Asn Lys Val His
74                  80                  85                  90
76 gct atc ccg ctg cgt tcc tcc tgg gtc atg acc tgt gcc tat gca cca   398
77 Ala Ile Pro Leu Arg Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro
78                  95                 100                 105
80 tca ggg aac ttc gtg gca tgt ggg ggg cta gat aac atg tgc tca atc   446
81 Ser Gly Asn Phe Val Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile
82             110                 115                 120
84 tac agc ctc aaa tcc cgt gag ggc aat gtc aag gtc agc cgg gaa ctc   494
85 Tyr Ser Leu Lys Ser Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu
86         125                 130                 135
88 tcg gct cac aca ggt tat ctc tcc tgt tgc cgc ttc ctg gat gac aac   542
89 Ser Ala His Thr Gly Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn
90 140                 145                 150                 155
92 aac att gtg act agc tct ggg gac acc acg tgt gcc ttg tgg gac att   590
93 Asn Ile Val Thr Ser Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile
94                 160                 165                 170
96 gag acg ggg cag cag aag aca gtg ttc gtg gga cac act ggt gac tgc   638
97 Glu Thr Gly Gln Gln Lys Thr Val Phe Val Gly His Thr Gly Asp Cys
98             175                 180                 185
100 atg agc ctg gct gtg tcc cca gac tac aaa ctc ttc atc tcg gga gct   686
101 Met Ser Leu Ala Val Ser Pro Asp Tyr Lys Leu Phe Ile Ser Gly Ala
102         190                 195                 200
104 tgt gat gcc agc gcc aag ctc tgg gat gtg agg gaa ggg acc tgt cgc   734
105 Cys Asp Ala Ser Ala Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg
106     205                 210                 215
108 cag act ttc act ggc cac gag tca gac atc aat gct atc tgt ttc ttt   782
109 Gln Thr Phe Thr Gly His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe
110 220                 225                 230                 235
112 ccc aat ggg gag gcc atc tgc act ggc tca gat gat gcc tcc tgc cgc   830
113 Pro Asn Gly Glu Ala Ile Cys Thr Gly Ser Asp Asp Ala Ser Cys Arg
114                 240                 245                 250
116 ctc ttt gac ctg agg gca gac cag gaa ctg aca gcc tac tcc cac gag   878
117 Leu Phe Asp Leu Arg Ala Asp Gln Glu Leu Thr Ala Tyr Ser His Glu
118             255                 260                 265
120 agc atc atc tgt ggc atc acg tcc gta gcc ttc tca ctc agt ggt cgc   926
121 Ser Ile Ile Cys Gly Ile Thr Ser Val Ala Phe Ser Leu Ser Gly Arg
122         270                 275                 280
124 ctg ctc ttt gct ggc tat gat gac ttc aac tgc aat gtc tgg gac tct   974
125 Leu Leu Phe Ala Gly Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ser
126     285                 290                 295
128 ctg aag tgt gag cgt gta ggc gtt ctt tct ggc cat gac aac aga gtc   1022
129 Leu Lys Cys Glu Arg Val Gly Val Leu Ser Gly His Asp Asn Arg Val
130 300                 305                 310                 315
132 agt tgc ctg ggg gtc aca gct gac ggc atg gct gtg gcc act gga tcc   1070
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137 Trp Asp Ser Phe Leu Lys Ile Trp Asn
138             335                 340
140 gtgggaagcc atgaaggctc tcagctgact cctatgccct gtctccttag ggtcagtctt 1177
142 ctataccctg gggccactcc cagtaaactt ccttctaagg gcaggtgggg ttataggagt 1237
144 gtgcctttgg gagtagcagg gtcacaaggg caaagaactg ccccatttcc tccagggcct 1297
146 ctcctctcca cagtcctcat agcttctccc ttcataaaca agaacagacc ctccccaccc 1357
148 tagatgactc ctgggctacc agcagcgttt gtccggcctg ggaatggcca gagcgctcag 1417
150 cccatgacta taggtgtcac tcctagtatc ctggctccct cccagcgact ttctttctgc 1477
152 ccttttgttc tctcttatta cctaataaaa tgtagcatcc tgg                    1520
155 <210> SEQ ID NO: 3
156 <211> LENGTH: 340
157 <212> TYPE: PRT
158 <213> ORGANISM: Rattus sp.
160 <400> SEQUENCE: 3
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162   1               5                  10                  15
164 Gln Ile Ala Asp Ala Arg Lys Ala Cys Ala Asp Ile Thr Leu Ala Glu
165             20                  25                  30
167 Leu Val Ser Gly Leu Glu Val Val Gly Arg Val Gln Met Arg Thr Arg
168         35                  40                  45
170 Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His Trp Ala
171     50                  55                  60
173 Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Gln Asp Gly Lys Leu Ile
174 65                  70                  75                  80
176 Val Trp Asp Thr Tyr Thr Thr Asn Lys Val His Ala Ile Pro Leu Arg
177                 85                  90                  95
179 Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Asn Phe Val
180             100                 105                 110
182 Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile Tyr Ser Leu Lys Ser
183         115                 120                 125
185 Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu Ser Ala His Thr Gly
186     130                 135                 140
188 Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Asn Ile Val Thr Ser
189 145                 150                 155                 160
191 Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile Glu Thr Gly Gln Gln
192                 165                 170                 175
194 Lys Thr Val Phe Val Gly His Thr Gly Asp Cys Met Ser Leu Ala Val
195             180                 185                 190
197 Ser Pro Asp Tyr Lys Leu Phe Ile Ser Gly Ala Cys Asp Ala Ser Ala
198         195                 200                 205
200 Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg Gln Thr Phe Thr Gly
201     210                 215                 220
203 His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe Pro Asn Gly Glu Ala
204 225                 230                 235                 240
206 Ile Cys Thr Gly Ser Asp Asp Ala Ser Cys Arg Leu Phe Asp Leu Arg
207                 245                 250                 255
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Input Set : A:\Pto.amc
Output Set: N:\CRF3\12182000\I492029.raw

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209 Ala Asp Gln Glu Leu Thr Ala Tyr Ser His Glu Ser Ile Ile Cys Gly
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212 Ile Thr Ser Val Ala Phe Ser Leu Ser Gly Arg Leu Leu Phe Ala Gly
213         275                 280                 285
215 Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ser Leu Lys Cys Glu Arg
216     290                 295                 300
218 Val Gly Val Leu Ser Gly His Asp Asn Arg Val Ser Cys Leu Gly Val
219 305                 310                 315                 320
221 Thr Ala Asp Gly Met Ala Val Ala Thr Gly Ser Trp Asp Ser Phe Leu
222                 325                 330                 335
224 Lys Ile Trp Asn
225             340
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230 <211> LENGTH: 1523
231 <212> TYPE: DNA
232 <213> ORGANISM: Homo sapiens
234 <220> FEATURE:
235 <221> NAME/KEY: CDS
236 <222> LOCATION: (7)..(1029)
237 <223> OTHER INFORMATION: human taste cell specific G-protein beta 3 subunit
239 <400> SEQUENCE: 4
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241         Met Gly Glu Met Glu Gln Leu Arg Gln Glu Ala Glu Gln Leu
242           1               5                  10
244 aag aag cag att gca gat gcc agg aaa gcc tgt gct gac gtt act ctg    96
245 Lys Lys Gln Ile Ala Asp Ala Arg Lys Ala Cys Ala Asp Val Thr Leu
246  15                  20                  25                  30
248 gca gag ctg gtg tct ggc cta gag gtg gtg gga cga gtc cag atg cgg   144
249 Ala Glu Leu Val Ser Gly Leu Glu Val Val Gly Arg Val Gln Met Arg
250                 35                  40                  45
252 acg cgg cgg acg tta agg gga cac ctg gcc aag att tac gcc atg cac   192
253 Thr Arg Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His
254             50                  55                  60
256 tgg gcc act gat tct aag ctg ctg gta agt gcc tcg caa gat ggg aag   240
257 Trp Ala Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Gln Asp Gly Lys
258         65                  70                  75
260 ctg atc gtg tgg gac agc tac acc acc aac aag gtg cac gcc atc cca   288
261 Leu Ile Val Trp Asp Ser Tyr Thr Thr Asn Lys Val His Ala Ile Pro
262     80                  85                  90
264 ctg cgc tcc tcc tgg gtc atg acc tgt gcc tat gcc cca tca ggg aac   336
265 Leu Arg Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Asn
266  95                 100                 105                 110
268 ttt gtg gca tgt ggg ggg ctg gac aac atg tgt tcc atc tac aac ctc   384
269 Phe Val Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile Tyr Asn Leu
270                 115                 120                 125
272 aaa tcc cgt gag ggc aat gtc aag gtc agc cgg gag ctt tct gct cac   432
273 Lys Ser Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu Ser Ala His
274             130                 135                 140
276 aca ggt tat ctc tcc tgc tgc cgc ttc ctg gat gac aac aat att gtg   480
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278 145 150 155
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281 Thr Ser Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile Glu Thr Gly
282 160 165 170
284 cag cag aag act gta ttt gtg gga cac acg ggt gac tgc atg agc ctg 576
285 Gln Gln Lys Thr Val Phe Val Gly His Thr Gly Asp Cys Met Ser Leu
286 175 180 185 190
288 gct gtg tct cct gac ttc aat ctc ttc att tcg ggg gcc tgt gat gcc 624
289 Ala Val Ser Pro Asp Phe Asn Leu Phe Ile Ser Gly Ala Cys Asp Ala
290 195 200 205
292 agt gcc aag ctc tgg gat gtg cga gag qgg acc tgc cgt cag act ttc 672
293 Ser Ala Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg Gln Thr Phe
294 210 215 220
296 act ggc cac gag tcg gac atc aac gcc atc tgt ttc ttc ccc aat gga 720
297 Thr Gly His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe Pro Asn Gly
298 225 230 235
300 gag gcc atc tgc acg ggc tcg gat gac gct tcc tgc cgc ttg ttt gac 768
301 Glu Ala Ile Cys Thr Gly Ser Asp Asp Ala Ser Cys Arg Leu Phe Asp
302 240 245 250
304 ctg cgg gca gac cag gag ctg atc tgc ttc tcc cac gag agc atc atc 816
305 Leu Arg Ala Asp Gln Glu Leu Ile Cys Phe Ser His Glu Ser Ile Ile
306 255 260 265 270
308 tgc ggc atc acg tcc gtg gcc ttc tcc ctc agt ggc cgc cta cta ttc 864
309 Cys Gly Ile Thr Ser Val Ala Phe Ser Leu Ser Gly Arg Leu Leu Phe
310 275 280 285
312 gct ggc tac gac gac ttc aac tgc aat gtc tgg gac tcc atg aag tct 912
313 Ala Gly Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ser Met Lys Ser
314 290 295 300
316 gag cgt gtg ggc atc ctc tct ggc cac gat aac agg gtg agc tgc ctg 960
317 Glu Arg Val Gly Ile Leu Ser Gly His Asp Asn Arg Val Ser Cys Leu
318 305 310 315
320 gga gtc aca gct gac ggg atg gct gtg gcc aca ggt tcc tgg gac agc 1008
321 Gly Val Thr Ala Asp Gly Met Ala Val Ala Thr Gly Ser Trp Asp Ser
322 320 325 330
324 ttc ctc aaa atc tgg aac tgaggaggct ggagaaaggg aagtggaagg 1056
325 Phe Leu Lys Ile Trp Asn
326 335 340
328 cagtgaacac actcagcagc cccctgcccg accccatctc attcaggtgt tctcttctat 1116
330 attccgggtg ccattcccac taagctttct cctttgaggg cagtgggggag catgggactg 1176
332 tgcctttggg aggcagcatc agggacacag gggcaaagaa ctgccccatc tcctcccatg 1236
334 gccttcctc cccacagtcc tcacagcctc tcccttaatg agcaaggaca acctgccccc 1296
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345 <210> SEQ ID NO: 5
346 <211> LENGTH: 340
347 <212> TYPE: PRT

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/492,029

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